

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Margolis, Benjamin L.
- (ii) TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATMENT OF BREAST CANCER
- (iii) NUMBER OF SEQUENCES: 21
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: PENNIE & EDMONDS LLP
 - (B) STREET: 1155 Avenue of the Americas
 - (C) CITY: New York
 - (D) STATE: New York
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 10036-2711
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/207,575
 - (B) FILING DATE: 07-MAR-1994
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Coruzzi, Laura A.
 - (B) REGISTRATION NUMBER: 30,742
 - (C) REFERENCE/DOCKET NUMBER: 7683-053
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (212) 790-9090
 - (B) TELEFAX: (212) 869-9741/8864
 - (C) TELEX: 66141 PENNIE

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
Gly Xaa Gly Xaa Xaa Gly
1 5

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Val Ala Val Lys
1

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Gly Met Xaa Tyr Leu
1 5

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ile His Arg Asp Leu Ala Ala Arg Asn
1 5

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Lys Trp Met Ala Pro Glu
1 5

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Lys Trp Thr Ala Pro Glu
1 5

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Phe Trp Tyr Ala Pro Glu
1 5

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ser Asp Val Trp Ser Phe Gly
1 5

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 334 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Arg Asp Ser Ser Arg Leu Cys Val Val Lys Val Tyr Ser Glu Asp Gly
1 5 10 15
Ala Cys Arg Ser Val Glu Val Ala Ala Gly Ala Thr Ala Arg His Val
20 25 30
Cys Glu Met Leu Val Gln Arg Ala His Ala Leu Ser Asp Glu Ser Trp
35 40 45
Gly Leu Val Glu Ser His Pro Tyr Leu Ala Leu Glu Arg Gly Leu Glu
50 55 60
Asp His Glu Phe Val Val Glu Val Gln Glu Ala Trp Pro Val Gly Gly
65 70 75 80
Asp Ser Arg Phe Ile Phe Arg Lys Asn Phe Ala Lys Tyr Glu Leu Phe
85 90 95
Lys Ser Pro Pro His Thr Leu Phe Pro Glu Lys Met Val Ser Ser Cys
100 105 110
Leu Asp Ala Gln Thr Gly Ile Ser His Glu Asp Leu Ile Gln Asn Phe
115 120 125
Leu Asn Ala Gly Ser Phe Pro Glu Ile Gln Gly Phe Leu Gln Leu Arg

130	135	140
Gly Ser Gly Arg Gly Ser Gly Arg Lys Leu Trp Lys Arg Phe Phe Cys 145 150 155 160		
Phe Leu Arg Arg Ser Gly Leu Tyr Tyr Ser Thr Lys Gly Thr Ser Lys 165 170 175		
Asp Pro Arg His Leu Gln Tyr Val Ala Asp Val Asn Glu Ser Asn Val 180 185 190		
Tyr Val Val Thr Gln Gly Arg Lys Leu Tyr Gly Met Pro Thr Asp Phe 195 200 205		
Gly Phe Cys Val Lys Pro Asn Lys Leu Arg Asn Gly His Lys Gly Leu 210 215 220		
His Ile Phe Cys Ser Glu Asp Glu Gln Ser Arg Thr Cys Trp Leu Ala 225 230 235 240		
Ala Phe Arg Leu Phe Lys Tyr Gly Val Gln Leu Tyr Lys Asn Tyr Gln 245 250 255		
Gln Ala Gln Ser Arg His Leu Arg Leu Ser Tyr Leu Gly Ser Pro Pro 260 265 270		
Leu Arg Ser Val Ser Asp Asn Thr Leu Val Ala Met Asp Phe Ser Gly 275 280 285		
His Ala Gly Arg Val Ile Asp Asn Pro Arg Glu Ala Leu Ser Ala Ala 290 295 300		
Met Glu Glu Ala Gln Ala Trp Arg Lys Lys Thr Asn His Arg Leu Ser 305 310 315 320		
Leu Pro Thr Thr Cys Ser Gly Ser Ser Leu Ser Ala Ala Ile 325 330		

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Lys Glu Ala Lys Val Thr Lys Ile Phe Val Lys Phe Phe Val Glu Asp 1 5 10 15
Gly Glu Ala Leu Gln Leu Leu Ile Asp Glu Arg Trp Thr Val Ala Asp 20 25 30
Thr Leu Lys Gln Leu Ala Glu Lys Asn His Ile Ala Leu Met Glu Asp 35 40 45
His Cys Ile Val Glu Glu Tyr Pro Glu Leu Tyr Ile Lys Arg Val Tyr 50 55 60
Glu Asp His Glu Lys Val Val Glu Asn Ile Gln Met Trp Val Gln Asp 65 70 75 80
Ser Pro Asn Lys Leu Tyr Phe Met Arg Arg Pro Asp Lys Tyr Ala Phe

85										90					95				
Ile	Ser	Arg	Pro	Glu	Leu	Tyr	Leu	Leu	Thr	Pro	Lys	Thr	Ser	Asp	His				
			100					105					110						
Met	Glu	Ile	Pro	Ser	Gly	Asp	Gln	Trp	Thr	Ile	Asp	Val	Lys	Gln	Lys				
		115					120					125							
Phe	Val	Ser	Glu	Tyr	Phe	His	Arg	Glu	Pro	Val	Val	Pro	Pro	Glu	Met				
	130					135					140								
Glu	Gly	Phe	Leu	Tyr	Leu	Lys	Ser	Asp	Gly	Arg	Lys	Ser	Trp	Lys	Lys				
145					150					155					160				
His	Tyr	Phe	Val	Leu	Arg	Pro	Ser	Gly	Leu	Tyr	Tyr	Ala	Pro	Lys	Ser				
				165					170					175					
Lys	Lys	Pro	Thr	Thr	Lys	Asp	Leu	Thr	Cys	Leu	Met	Asn	Leu	His	Ser				
			180					185					190						
Asn	Gln	Val	Tyr	Thr	Gly	Ile	Gly	Trp	Glu	Lys	Lys	Tyr	Lys	Ser	Pro				
		195					200					205							
Thr	Pro	Trp	Cys	Ile	Ser	Ile	Lys	Leu	Thr	Ala	Leu	Gln	Met	Lys	Arg				
	210					215					220								
Ser	Gln	Phe	Ile	Lys	Tyr	Ile	Cys	Ala	Glu	Asp	Glu	Met	Thr	Phe	Lys				
225					230					235					240				
Lys	Trp	Leu	Val	Ala	Leu	Arg	Ile	Ala	Lys	Asn	Gly	Ala	Glu	Leu	Leu				
				245					250					255					
Glu	Asn	Tyr	Glu	Arg	Ala	Cys	Gln	Ile	Arg	Arg	Glu	Thr	Leu	Gly	Pro				
			260					265					270						
Ala	Ser	Ser	Met	Ser	Ala	Ala	Ser	Ser	Ser	Thr	Ala	Ile	Ser	Glu	Val				
		275					280				285								
Pro	His	Ser	Leu	Ser	His	His	Gln	Arg	Thr	Pro	Ser	Val	Ala	Ser	Ser				
	290					295					300								
Ile	Gln	Leu	Ser	Ser	His	Met	Met	Asn	Asn	Pro	Thr	His	Pro	Leu	Ser				
305					310					315					320				
Val	Asn	Val	Arg	Asn	Gln	Ser	Pro	Ala	Ser	Phe	Ser	Val	Asn	Ser	Cys				
				325					330				335						
Gln	Gln	Ser	His	Pro	Ser	Arg	Thr	Ser	Ala	Lys	Leu								
			340					345											

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1, 25-27, 32, 46, 47, 49, 52, 54, 72, 75, 77, 93, 95, 105, 107, 108 and 111
- (D) OTHER INFORMATION: /label= Xaa
/note= "Xaa at these positions = Hydrophobic"

residues"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2, 21, 23 and 101
- (D) OTHER INFORMATION: /label= Xaa
/note= "Xaa at these positions = Basic residues"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3, 7, 9, 11-19, 22, 28-31, 36-42, 44, 48
50, 51, 53, 55-70, 74, 76, 78-90, 92, 94
96-98, 106 109 and 110
- (D) OTHER INFORMATION: /label= Xaa
/note= "Xaa at these positions = Non-consensus
residues"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 24, 33-35 and 91
- (D) OTHER INFORMATION: /label= Xaa
/note= "Xaa at these positions = Aromatic
residues"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 99, 100, 102 and 103
- (D) OTHER INFORMATION: /label= Xaa
/note= "Xaa at these positions = Acidic residues"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Xaa	Xaa	Xaa	Gly	Phe	Leu	Xaa	Lys	Xaa	Gly	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
1				5					10						15	
Xaa	Xaa	Xaa	Trp	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			20					25						30		
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Pro	Xaa	Gly	Xaa	Xaa	Xaa	Xaa
			35					40				45				
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			50				55					60				
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Asn	Xaa	Phe	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
65					70				75							80
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
				85					90						95	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Trp	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
				100				105							110	

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1

- (D) OTHER INFORMATION: /label= Xaa
/note= "Xaa = Isoleucine or Valine"
- (ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 2, 69 and 102
(D) OTHER INFORMATION: /label= Xaa
/note= "Xaa at these positions = Arginine or Lysine"
- (ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 5
(D) OTHER INFORMATION: /label= Xaa
/note= "Xaa = Tyrosine or Tryptophan"
- (ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 7, 11-17, 22, 28, 29, 31, 33, 35, 38-42
46, 47, 50-52, 58-68, 70, 72, 74, 76-78
80-92, 96, 98, 109, 110
(D) OTHER INFORMATION: /label= Xaa
/note= "Xaa at these positions = Non-consensus residues"
- (ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 8, 9, 18 and 21
(D) OTHER INFORMATION: /label= Xaa
/note= "Xaa at these positions = Lysine or Arginine"
- (ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 19
(D) OTHER INFORMATION: /label= Xaa
/note= "Xaa = Threonine or Serine"
- (ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 24
(D) OTHER INFORMATION: /label= Xaa
/note= "Xaa = Tryptophan or Tyrosine"
- (ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 26 and 57
(D) OTHER INFORMATION: /label= Xaa
/note= "Xaa at these positions = Valine or Isoleucine"
- (ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 30
(D) OTHER INFORMATION: /label= Xaa
/note= "Xaa = Aspartic Acid or Glycine"
- (ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 34
(D) OTHER INFORMATION: /label= Xaa
/note= "Xaa = Leucine or Tyrosine"
- (ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 36
(D) OTHER INFORMATION: /label= Xaa

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        /note= "Xaa = Tyrosine or Phenylalanine"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 37
    (D) OTHER INFORMATION: /label= Xaa
        /note= "Xaa = Lysine or Glutamic Acid"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 55
    (D) OTHER INFORMATION: /label= Xaa
        /note= "Xaa = Cysteine or Valine"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 56
    (D) OTHER INFORMATION: /label= Xaa
        /note= "Xaa = Glutamine or Glutamic Acid"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 71
    (D) OTHER INFORMATION: /label= Xaa
        /note= "Xaa = Asparagine or Histidine"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 75 and 108
    (D) OTHER INFORMATION: /label= Xaa
        /note= "Xaa at these positions = Isoleucine
        or Leucine"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 93
    (D) OTHER INFORMATION: /label= Xaa
        /note= "Xaa = Phenylalanine or Leucine"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 94
    (D) OTHER INFORMATION: /label= Xaa
        /note= "Xaa = Glutamine or Alanine"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 97
    (D) OTHER INFORMATION: /label= Xaa
        /note= "Xaa = Serine or Threonine"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 102 and 103
    (D) OTHER INFORMATION: /label= Xaa
        /note= "Xaa at these positions = Glutamic Acid
        or Aspartic Acid"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 105
    (D) OTHER INFORMATION: /label= Xaa
        /note= "Xaa = Valine or Methionine"

(ix) FEATURE:
    (A) NAME/KEY: Modified-site
    (B) LOCATION: 111

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(D) OTHER INFORMATION: /label= Xaa
/note= "Xaa = Alanine or Valine"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Ile Arg Glu Gly Tyr Leu Xaa Lys Lys Gly Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15
Xaa Lys Thr Trp Lys Xaa Arg Trp Phe Val Leu Xaa Xaa Asp Xaa Leu
20 25 30
Xaa Leu Xaa Tyr Lys Xaa Xaa Xaa Xaa Xaa Pro Lys Gly Xaa Xaa Pro
35 40 45
Leu Xaa Xaa Xaa Ser Val Cys Gln Val Xaa Xaa Xaa Xaa Xaa Xaa
50 55 60
Xaa Xaa Xaa Xaa Arg Xaa Asn Xaa Phe Xaa Ile Xaa Xaa Xaa Asp Xaa
65 70 75 80
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Gln Ala Xaa
85 90 95
Ser Xaa Glu Glu Arg Glu Glu Trp Val Lys Ala Ile Xaa Xaa Ala
100 105 110

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Asp Leu Arg Ala Ala Asn
1 5

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 2
(D) OTHER INFORMATION: /label= Xaa
/note= "Xaa = Isoleucine or Valine"

(ix) FEATURE:

(A) NAME/KEY: Modified-site
(B) LOCATION: 3
(D) OTHER INFORMATION: /label= Xaa
/note= "Xaa = Lysine or Arginine"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

- (B) LOCATION: 5
- (D) OTHER INFORMATION: /label= Xaa
/note= "Xaa = Threonine or Methionine"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Pro Xaa Xaa Trp Xaa Ala Pro Glu
1 5

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /label= Xaa
/note= "Xaa = Valine or Isoleucine"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 7
- (D) OTHER INFORMATION: /label= Xaa
/note= "Xaa = Valine or Isoleucine"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Xaa Pro Xaa Tyr Xaa Asn Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 8
- (D) OTHER INFORMATION: /label= Xaa
/note= "Xaa = Hydrophobic Residue"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Xaa Pro Xaa Xaa Pro Pro Pro Xaa Xaa Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Pro Pro Val Pro Pro Arg Arg
1 5

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Asp Leu Arg Ala Ala Asn
1 5

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Asp Leu Ala Ala Arg Asn
1 5

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Phe Leu Ile Arg Glu Ser
1 5

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Phe Leu Val Arg Glu Ser
1 5